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1638

RAW SEQUENCE LISTING

DATE: 04/08/2002

PATENT APPLICATION: US/09/534,861A

TIME: 16:09:37

Input Set : A:\15313SEQ.txt

Output Set: N:\CRF3\04082002\1534861A.raw

P.S

3 <110> APPLICANT: Smeekens, J.C.M.
 4 Ebskamp, Michael
 5 Geerts, Hendrikis
 6 Weisbeek, Petrus
 8 <120> TITLE OF INVENTION: Production of Oligosaccharides in Transgenic Plants
 10 <130> FILE REFERENCE: ARNO-1-15313
 C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/534,861A
 13 <141> CURRENT FILING DATE: 2000-03-24
 15 <150> PRIOR APPLICATION NUMBER: US 09/019,385
 16 <151> PRIOR FILING DATE: 1998-02-05
 18 <150> PRIOR APPLICATION NUMBER: US 09/193,385
 19 <151> PRIOR FILING DATE: 1998-11-17
 21 <150> PRIOR APPLICATION NUMBER: US 08/479,470
 22 <151> PRIOR FILING DATE: 1995-06-07
 24 <150> PRIOR APPLICATION NUMBER: NL 1000064
 25 <151> PRIOR FILING DATE: 1995-04-05
 27 <150> PRIOR APPLICATION NUMBER: NL 9401140
 28 <151> PRIOR FILING DATE: 1994-08-07
 30 <160> NUMBER OF SEQ ID NOS: 12
 32 <170> SOFTWARE: PatentIn version 3.0
 34 <210> SEQ ID NO: 1
 35 <211> LENGTH: 2094
 36 <212> TYPE: DNA
 37 <213> ORGANISM: Barley
 39 <220> FEATURE:
 40 <221> NAME/KEY: CDS
 41 <222> LOCATION: (46)..(1923)
 43 <400> SEQUENCE: 1
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 45 Met Gly Ser His
 46 1
 48 ggc aag cca ccg cta ccg tac gcc tac aag ccg ctg ccc tcg gac gcc 105
 49 Gly Lys Pro Pro Leu Pro Tyr Ala Tyr Lys Pro Leu Pro Ser Asp Ala
 50 5 10 15 20
 52 gcc gac ggt aag ccg acc ggc tgc atg agg tgg tcc gcg tgt gcc acc 153
 53 Ala Asp Gly Lys Arg Thr Gly Cys Met Arg Trp Ser Ala Cys Ala Thr
 54 25 30 35
 56 gtg ctg acg gcc tcg gcc atg gcg gtg gtg gtg gtc gcc gcc acg ctc 201
 57 Val Leu Thr Ala Ser Ala Met Ala Val Val Val Gly Ala Thr Leu
 58 40 45 50
 60 ctg gcg gga ttg agg atg gag cag gcc gtc gac gag gag gcg gcg gcg 249
 61 Leu Ala Gly Leu Arg Met Glu Gln Ala Val Asp Glu Glu Ala Ala Ala
 62 55 60 65

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64 ggc ggg ttc ccg tgg agc aac gag atg ctg cag tgg cag cgc agc ggt      297
65 Gly Gly Phe Pro Trp Ser Asn Glu Met Leu Gln Trp Gln Arg Ser Gly
66      70      75      80
68 tac cat ttc cag acg gcc aag aac tac atg agc gat ccc aac ggc ctg      345
69 Tyr His Phe Gln Thr Ala Lys Asn Tyr Met Ser Asp Pro Asn Gly Leu
70 85      90      95      100
72 atg tat tac cgt gga tgg tac cac atg ttc tac cag tac aac ccg gtg      393
73 Met Tyr Tyr Arg Gly Trp Tyr His Met Phe Tyr Gln Tyr Asn Pro Val
74      105      110      115
76 ggc acc gac tgg gac gac ggc atg gag tgg ggc cac gcc gtg tcc cgg      441
77 Gly Thr Asp Trp Asp Asp Gly Met Glu Trp Gly His Ala Val Ser Arg
78      120      125      130
80 aac ctt gtc caa tgg cgc acc ctc cct atc gcc atg gtg gcc gac cag      489
81 Asn Leu Val Gln Trp Arg Thr Leu Pro Ile Ala Met Val Ala Asp Gln
82      135      140      145
84 tgg tac gac atc ctc gga gtc ctc tcg ggc tcc atg acg gtg cta ccc      537
85 Trp Tyr Asp Ile Leu Gly Val Leu Ser Gly Ser Met Thr Val Leu Pro
86      150      155      160
88 aac ggg acg gtc atc atg atc tac acg ggc gcc acc aac gcc tcc gcc      585
89 Asn Gly Thr Val Ile Met Ile Tyr Thr Gly Ala Thr Asn Ala Ser Ala
90 165      170      175      180
92 gtg gag gtc cag tgc atc gcc acc ccg gcc gac ccc aac gac ccc ctc      633
93 Val Glu Val Gln Cys Ile Ala Thr Pro Ala Asp Pro Asn Asp Pro Leu
94      185      190      195
96 ctc cgc cgg tgg acc aag cac ccc gcc aac ccc gtc atc tgg tcg ccg      681
97 Leu Arg Arg Trp Thr Lys His Pro Ala Asn Pro Val Ile Trp Ser Pro
98      200      205      210
100 ccg ggg gtc ggc acc aag gat ttc cga gac ccg atg acc gcc tgg tac      729
101 Pro Gly Val Gly Thr Lys Asp Phe Arg Asp Pro Met Thr Ala Trp Tyr
102      215      220      225
104 gac gag tcc gac gag aca tgg cgc acc ctc ctc ggg tcc aag gac gac      777
105 Asp Glu Ser Asp Glu Thr Trp Arg Thr Leu Leu Gly Ser Lys Asp Asp
106      230      235      240
108 cac gac ggc cac cac gac ggc atc gcc atg atg tac aag acc aag gac      825
109 His Asp Gly His His Asp Gly Ile Ala Met Met Tyr Lys Thr Lys Asp
110 245      250      255      260
112 ttc ctc aac tac gag ctc atc ccg ggc atc ttg cac cgg gtg gtg cgc      873
113 Phe Leu Asn Tyr Glu Leu Ile Pro Gly Ile Leu His Arg Val Val Arg
114      265      270      275
116 acc ggc gag tgg gag tgc atc gac ttc tac ccc gtc ggc cgg aga agc      921
117 Thr Gly Glu Trp Glu Cys Ile Asp Phe Tyr Pro Val Gly Arg Arg Ser
118      280      285      290
120 agc gac aac tcg tcg gag atg ctg cac gtg ttg aag gcg agc atg gac      969
121 Ser Asp Asn Ser Ser Glu Met Leu His Val Leu Lys Ala Ser Met Asp
122      295      300      305
124 gac gaa cgg cac gac tac tac tcg ctg ggc acg tac gac tcg gcg gcc      1017
125 Asp Glu Arg His Asp Tyr Trp Ser Leu Gly Thr Tyr Asp Ser Ala Ala
126      310      315      320
128 aac acg tgg acg ccc atc gac ccg gag ctc gac ttg ggg atc ggg ctg      1065

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129 Asn Thr Trp Thr Pro Ile Asp Pro Glu Leu Asp Leu Gly Ile Gly Leu
130 325 330 335 340
132 aga tac gac tgg gga aag ttt tat gcg tcc acc tcc ttc tat gat ccg 1113
133 Arg Tyr Asp Trp Gly Lys Phe Tyr Ala Ser Thr Ser Phe Tyr Asp Pro
134 345 350 355
136 gcc aag aac cgg cgc gtg ctc atg ggg tac gtc ggc gag gtc gac tcc 1161
137 Ala Lys Asn Arg Arg Val Leu Met Gly Tyr Val Gly Glu Val Asp Ser
138 360 365 370
140 aag cgg gct gat gtc gtc aag gga tgg gct tcc att cag tca gtt cct 1209
141 Lys Arg Ala Asp Val Val Lys Gly Trp Ala Ser Ile Gln Ser Val Pro
142 375 380 385
144 agg acg gtg gct ctg gat gag aag acc cgg acg aac ctc ctg ctc tgg 1257
145 Arg Thr Val Ala Leu Asp Glu Lys Thr Arg Thr Asn Leu Leu Leu Trp
146 390 395 400
148 ccc gtt gag gag atc gag acc ctc cgc ctc aat gcc acg gaa ctg acc 1305
149 Pro Val Glu Glu Ile Glu Thr Leu Arg Leu Asn Ala Thr Glu Leu Thr
150 405 410 415 420
152 gac gtt acc att aac act ggc tcc gtc atc cat atc ccg ctc cgc caa 1353
153 Asp Val Thr Ile Asn Thr Gly Ser Val Ile His Ile Pro Leu Arg Gln
154 425 430 435
156 ggc act cac gct cga cat gcg gag gcc tct ttc cac ctt gat gct tcc 1401
157 Gly Thr His Ala Arg His Ala Glu Ala Ser Phe His Leu Asp Ala Ser
158 440 445 450
160 gcc gtg gct gcc ctc aac gag gcc gat gtg ggc tac aac tgc agt agc 1449
161 Ala Val Ala Ala Leu Asn Glu Ala Asp Val Gly Tyr Asn Cys Ser Ser
162 455 460 465
164 agc ggc ggc gct gtt aac cgc ggc gcg cta ggc ccc ttc ggc ctc ctc 1497
165 Ser Gly Gly Ala Val Asn Arg Gly Ala Leu Gly Pro Phe Gly Leu Leu
166 470 475 480
168 gtc ctc gcc gcc ggt gac cgc cgt ggc gag caa acg gcg gtc tac ttc 1545
169 Val Leu Ala Ala Gly Asp Arg Arg Gly Glu Gln Thr Ala Val Tyr Phe
170 485 490 495 500
172 tac gtg tct agg ggc ctt gac gga ggc ctc cac acc agc ttc tgc caa 1593
173 Tyr Val Ser Arg Gly Leu Asp Gly Gly Leu His Thr Ser Phe Cys Gln
174 505 510 515
176 gat gag ctg aga tcg tca cga gcc aag gat gtg acc aag cgt gtc atc 1641
177 Asp Glu Leu Arg Ser Ser Arg Ala Lys Asp Val Thr Lys Arg Val Ile
178 520 525 530
180 ggg agc acg gtg ccg gtg ctc gac ggt gag gct ttg tca atg agg gtg 1689
181 Gly Ser Thr Val Pro Val Leu Asp Gly Glu Ala Leu Ser Met Arg Val
182 535 540 545
184 ctc gtg gat cac tcc atc gtg cag ggc ttc gac atg ggc ggg agg acc 1737
185 Leu Val Asp His Ser Ile Val Gln Gly Phe Asp Met Gly Gly Arg Thr
186 550 555 560
188 acg atg acc tcg cgg gtg tac ccg atg gag tcg tat cag gag gca aga 1785
189 Thr Met Thr Ser Arg Val Tyr Pro Met Glu Ser Tyr Gln Glu Ala Arg
190 565 570 575 580
192 gtc tac ttg ttc aac aac gcc acc ggt gcc agc gtg acg gcg gaa agg 1833
193 Val Tyr Leu Phe Asn Asn Ala Thr Gly Ala Ser Val Thr Ala Glu Arg

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194          585          590          595
196 ctg gtc gtg cac gag atg gac tcg gca cac aac cag etc tcc aat gag      1881
197 Leu Val Val His Glu Met Asp Ser Ala His Asn Gln Leu Ser Asn Glu
198          600          605          610
200 gac gat ggc atg tat ctt cat caa gtt ctt gaa tct cgt cat      1923
201 Asp Asp Gly Met Tyr Leu His Gln Val Leu Glu Ser Arg His
202          615          620          625
204 taataagcta cattggatca aagaagatca ccagggaagg gcaattcata cataaatcga      1983
206 atcattctgc acaacctgc ttgcagcatg cattgaaaca tctgtatttg gatcatcttc      2043
208 ttcatttatg tcatagtga ctatattact ttgtaaaaaa aaaaaaaaaa a      2094
211 <210> SEQ ID NO: 2
212 <211> LENGTH: 626
213 <212> TYPE: PRT
214 <213> ORGANISM: Barley
216 <400> SEQUENCE: 2
218 Met Gly Ser His Gly Lys Pro Pro Leu Pro Tyr Ala Tyr Lys Pro Leu
219 1          5          10          15
222 Pro Ser Asp Ala Ala Asp Gly Lys Arg Thr Gly Cys Met Arg Trp Ser
223          20          25          30
226 Ala Cys Ala Thr Val Leu Thr Ala Ser Ala Met Ala Val Val Val Val
227          35          40          45
230 Gly Ala Thr Leu Leu Ala Gly Leu Arg Met Glu Gln Ala Val Asp Glu
231          50          55          60
234 Glu Ala Ala Ala Gly Gly Phe Pro Trp Ser Asn Glu Met Leu Gln Trp
235 65          70          75          80
238 Gln Arg Ser Gly Tyr His Phe Gln Thr Ala Lys Asn Tyr Met Ser Asp
239          85          90          95
242 Pro Asn Gly Leu Met Tyr Tyr Arg Gly Trp Tyr His Met Phe Tyr Gln
243          100          105          110
246 Tyr Asn Pro Val Gly Thr Asp Trp Asp Asp Gly Met Glu Trp Gly His
247          115          120          125
250 Ala Val Ser Arg Asn Leu Val Gln Trp Arg Thr Leu Pro Ile Ala Met
251          130          135          140
254 Val Ala Asp Gln Trp Tyr Asp Ile Leu Gly Val Leu Ser Gly Ser Met
255 145          150          155          160
258 Thr Val Leu Pro Asn Gly Thr Val Ile Met Ile Tyr Thr Gly Ala Thr
259          165          170          175
262 Asn Ala Ser Ala Val Glu Val Gln Cys Ile Ala Thr Pro Ala Asp Pro
263          180          185          190
266 Asn Asp Pro Leu Leu Arg Arg Trp Thr Lys His Pro Ala Asn Pro Val
267          195          200          205
270 Ile Trp Ser Pro Pro Gly Val Gly Thr Lys Asp Phe Arg Asp Pro Met
271          210          215          220
274 Thr Ala Trp Tyr Asp Glu Ser Asp Glu Thr Trp Arg Thr Leu Leu Gly
275 225          230          235          240
278 Ser Lys Asp Asp His Asp Gly His His Asp Gly Ile Ala Met Met Tyr
279          245          250          255
282 Lys Thr Lys Asp Phe Leu Asn Tyr Glu Leu Ile Pro Gly Ile Leu His
283          260          265          270

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286 Arg Val Val Arg Thr Gly Glu Trp Glu Cys Ile Asp Phe Tyr Pro Val
287          275          280          285
290 Gly Arg Arg Ser Ser Asp Asn Ser Ser Glu Met Leu His Val Leu Lys
291      290          295          300
294 Ala Ser Met Asp Asp Glu Arg His Asp Tyr Tyr Ser Leu Gly Thr Tyr
295 305          310          315          320
298 Asp Ser Ala Ala Asn Thr Trp Thr Pro Ile Asp Pro Glu Leu Asp Leu
299          325          330          335
302 Gly Ile Gly Leu Arg Tyr Asp Trp Gly Lys Phe Tyr Ala Ser Thr Ser
303          340          345          350
306 Phe Tyr Asp Pro Ala Lys Asn Arg Arg Val Leu Met Gly Tyr Val Gly
307          355          360          365
310 Glu Val Asp Ser Lys Arg Ala Asp Val Val Lys Gly Trp Ala Ser Ile
311      370          375          380
314 Gln Ser Val Pro Arg Thr Val Ala Leu Asp Glu Lys Thr Arg Thr Asn
315 385          390          395          400
318 Leu Leu Leu Trp Pro Val Glu Glu Ile Glu Thr Leu Arg Leu Asn Ala
319          405          410          415
322 Thr Glu Leu Thr Asp Val Thr Ile Asn Thr Gly Ser Val Ile His Ile
323          420          425          430
326 Pro Leu Arg Gln Gly Thr His Ala Arg His Ala Glu Ala Ser Phe His
327          435          440          445
330 Leu Asp Ala Ser Ala Val Ala Ala Leu Asn Glu Ala Asp Val Gly Tyr
331      450          455          460
334 Asn Cys Ser Ser Ser Gly Gly Ala Val Asn Arg Gly Ala Leu Gly Pro
335 465          470          475          480
338 Phe Gly Leu Leu Val Leu Ala Ala Gly Asp Arg Arg Gly Glu Gln Thr
339          485          490          495
342 Ala Val Tyr Phe Tyr Val Ser Arg Gly Leu Asp Gly Gly Leu His Thr
343          500          505          510
346 Ser Phe Cys Gln Asp Glu Leu Arg Ser Ser Arg Ala Lys Asp Val Thr
347      515          520          525
350 Lys Arg Val Ile Gly Ser Thr Val Pro Val Leu Asp Gly Glu Ala Leu
351      530          535          540
354 Ser Met Arg Val Leu Val Asp His Ser Ile Val Gln Gly Phe Asp Met
355 545          550          555          560
358 Gly Gly Arg Thr Thr Met Thr Ser Arg Val Tyr Pro Met Glu Ser Tyr
359          565          570          575
362 Gln Glu Ala Arg Val Tyr Leu Phe Asn Asn Ala Thr Gly Ala Ser Val
363          580          585          590
366 Thr Ala Glu Arg Leu Val Val His Glu Met Asp Ser Ala His Asn Gln
367          595          600          605
370 Leu Ser Asn Glu Asp Asp Gly Met Tyr Leu His Gln Val Leu Glu Ser
371      610          615          620
374 Arg His
375 625
378 <210> SEQ ID NO: 3
379 <211> LENGTH: 30
380 <212> TYPE: DNA

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FYI

VERIFICATION SUMMARY

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L:12 M:270 C: Current Application Number differs, Replaced Current Application Number
L:474 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:490 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12